



SEQUENCE LISTING

<110> Shaw, Jei-Fu
 Lee, Guan-Chiun
 Tang, Shye-Jye

<120> RECOMBINANT CANDIDA RUGOSA LIPASES

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<140> US 09/943,857

<141> 2001-08-31

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Leu Arg Phe Lys Pro Pro Val Pro Tyr Ser Ala Ser Leu Asn Gly Gln	
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Gln Phe Thr Ser Tyr Gly Pro Ser Cys Met Gln Met Asn Pro Met Gly	
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tcc aag atc ttc caa gtg gtg ctt ccc aac gac gag gac tgt ctc acc	336
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 Ser Lys Gln Leu Ser Gly Leu Pro Val Leu Gly Thr Phe His Gly Asn
 450 455 460
 Asp Ile Ile Trp Gln Asp Tyr Leu Val Gly Ser Gly Ser Val Ile Tyr
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 <213> *Candida rugosa*

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Ala	Glu	Ile	Asp	Thr	Leu	Met	Ala	Ala	Tyr	Pro	Gln	Asp	Ile	Thr	Gln
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Gly	Ser	Pro	Phe	Asp	Thr	Gly	Val	Leu	Asn	Ala	Leu	Thr	Pro	Gln	Phe

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 Arg Tyr Phe Leu Asn His Phe Gln Gly Gly Thr Lys Tyr Ser Phe Leu
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 Ser Lys Gln Leu Ser Gly Leu Pro Ile Met Gly Thr Phe His Ala Asn
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 Asp Ile Val Trp Gln Asp Tyr Leu Leu Gly Ser Gly Ser Val Ile Tyr
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<212> DNA

<213> *Candida rugosa*

<220>

<221> CDS

<222> (1) ... (1641)

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Leu	Arg	Phe	Lys	Pro	Pro	Val	Pro	Tyr	Ser	Ala	Ser	Leu	Asn	Gly	Gln	
		50				55					60					

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Lys	Phe	Thr	Ser	Tyr	Gly	Pro	Ser	Cys	Met	Gln	Met	Asn	Pro	Leu	Gly	
	65				70				75					80		

aac	tgg	gac	tcc	tcg	ctt	ccc	aag	gct	gcc	atc	aac	tcc	ttg	atg	cag	288
Asn	Trp	Asp	Ser	Ser	Leu	Pro	Lys	Ala	Ala	Ile	Asn	Ser	Leu	Met	Gln	
			85					90						95		

tcc	aag	ctc	ttc	cag	gcg	gtg	ctt	cct	aac	ggc	gag	gac	tgt	ctc	acc	336
Ser	Lys	Leu	Phe	Gln	Ala	Val	Leu	Pro	Asn	Gly	Glu	Asp	Cys	Leu	Thr	
			100				105						110			

atc aac gtg gtg cgg ccg tca ggc acc aag ccg ggt gcc aac ctc ccc Ile Asn Val Val Arg Pro Ser Gly Thr Lys Pro Gly Ala Asn Leu Pro 115 120 125	384
gtg atg gtg tgg att ttt ggc ggc ggg ttt gag gtt ggc ggc tcc agt Val Met Val Trp Ile Phe Gly Gly Gly Phe Glu Val Gly Gly Ser Ser 130 135 140	432
ctc ttc cct ccc gca cag atg atc acc gcc agc gtg ctt atg ggc aag Leu Phe Pro Pro Ala Gln Met Ile Thr Ala Ser Val Leu Met Gly Lys 145 150 155 160	480
ccc atc atc cac gtg agc atg aac tac cgc gtt gct tcg tgg ggg ttc Pro Ile Ile His Val Ser Met Asn Tyr Arg Val Ala Ser Trp Gly Phe 165 170 175	528
ttg gct ggt cca gac atc aag gcc gag ggc agc ggg aac gcc ggt ttg Leu Ala Gly Pro Asp Ile Lys Ala Glu Gly Ser Gly Asn Ala Gly Leu 180 185 190	576
cac gac caa cgc ttg ggt ttg cag tgg gtg gcg gac aac att gcc ggg His Asp Gln Arg Leu Gly Leu Gln Trp Val Ala Asp Asn Ile Ala Gly 195 200 205	624
ttc ggc ggc gac ccg tcc aag gtg acc atc ttt ggt gag tcg gcg ggc Phe Gly Gly Asp Pro Ser Lys Val Thr Ile Phe Gly Glu Ser Ala Gly 210 215 220	672
agc atg tcg gta atg tgt cag ctc ctc tgg aac gac ggc gac aac acg Ser Met Ser Val Met Cys Gln Leu Leu Trp Asn Asp Gly Asp Asn Thr 225 230 235 240	720
tac aac ggc aag ccg ttg ttc cgt gcc gcc atc atg cag tct ggg gcc Tyr Asn Gly Lys Pro Leu Phe Arg Ala Ala Ile Met Gln Ser Gly Ala 245 250 255	768
atg gtg ccg tcg gac ccg gtg gat ggg ccc tac ggc acg cag atc tac Met Val Pro Ser Asp Pro Val Asp Gly Pro Tyr Gly Thr Gln Ile Tyr 260 265 270	816
gac cag gtg gtt gct tca gcc ggc tgt ggc agt gcc agc gac aag ctc Asp Gln Val Val Ala Ser Ala Gly Cys Gly Ser Ala Ser Asp Lys Leu 275 280 285	864
gcg tgc ttg cgc agc atc tcg aac gac aaa ctc ttc cag gcc acc agc Ala Cys Leu Arg Ser Ile Ser Asn Asp Lys Leu Phe Gln Ala Thr Ser 290 295 300	912
gac act ccg ggg gcc ttg gcg tac ccc tcg ttg cgg ttg tcg ttt ctc Asp Thr Pro Gly Ala Leu Ala Tyr Pro Ser Leu Arg Leu Ser Phe Leu 305 310 315 320	960
ccg cgg ccc gac ggc acc ttc atc acc gat gac atg ttc aag ttg gtg Pro Arg Pro Asp Gly Thr Phe Ile Thr Asp Asp Met Phe Lys Leu Val 325 330 335	1008

cgc gac ggc aag tgt gcc aac gtt ccg gtg atc att ggc gac cag aac Arg Asp Gly Lys Cys Ala Asn Val Pro Val Ile Ile Gly Asp Gln Asn 340 345 350	1056
gac gag ggc aca gtg ttt gcg ttg tcc agc ttg aac gtg act acg gat Asp Glu Gly Thr Val Phe Ala Leu Ser Ser Leu Asn Val Thr Thr Asp 355 360 365	1104
gct cag gca cgc cag tac ttc aag gaa agc ttc atc cac gcc agc gac Ala Gln Ala Arg Gln Tyr Phe Lys Glu Ser Phe Ile His Ala Ser Asp 370 375 380	1152
gcg gag atc gac acc ttg atg gcg gcg tac ccc agc gac atc acc cag Ala Glu Ile Asp Thr Leu Met Ala Ala Tyr Pro Ser Asp Ile Thr Gln 385 390 395 400	1200
ggc agt ccg ttc gac acc ggc atc ttc aac gcc atc acc ccg cag ttc Gly Ser Pro Phe Asp Thr Gly Ile Phe Asn Ala Ile Thr Pro Gln Phe 405 410 415	1248
aaa cgg att gca gcg gtg ctt ggt gac ctt gcg ttc act ctc ccc cgg Lys Arg Ile Ala Ala Val Leu Gly Asp Leu Ala Phe Thr Leu Pro Arg 420 425 430	1296
cgc tac ttc ctc aac cac ttc cag ggc ggc acc aag tac tcg ttc ctc Arg Tyr Phe Leu Asn His Phe Gln Gly Gly Thr Lys Tyr Ser Phe Leu 435 440 445	1344
tcg aag cag ctt agt ggg ttg ccg gtg att ggc acc cac cac gcc aac Ser Lys Gln Leu Ser Gly Leu Pro Val Ile Gly Thr His His Ala Asn 450 455 460	1392
gac att gtg tgg cag gac ttt ttg gtg agc cac agc agc gcc gtg tac Asp Ile Val Trp Gln Asp Phe Leu Val Ser His Ser Ser Ala Val Tyr 465 470 475 480	1440
aac aac gcg ttt att gcc ttt gcc aac gac ctc gac ccg aac aag gcc Asn Asn Ala Phe Ile Ala Phe Ala Asn Asp Leu Asp Pro Asn Lys Ala 485 490 495	1488
ggc ttg ctt gtg aac tgg ccc aag tac acc agc agc tct cag tca ggc Gly Leu Leu Val Asn Trp Pro Lys Tyr Thr Ser Ser Ser Gln Ser Gly 500 505 510	1536
aac aac ttg ttg cag atc aac gcc ttg ggc ttg tac acc ggc aag gac Asn Asn Leu Leu Gln Ile Asn Ala Leu Gly Leu Tyr Thr Gly Lys Asp 515 520 525	1584
aac ttc cgc acc gct ggc tac gac gcg ttg ttt acc aac ccg tct tct Asn Phe Arg Thr Ala Gly Tyr Asp Ala Leu Phe Thr Asn Pro Ser Ser 530 535 540	1632
ttc ttt gtg Phe Phe Val 545	1641

<210> 6
 <211> 547
 <212> PRT
 <213> Candida rugosa

<400> 6
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 Ala Thr Leu Ala Asn Gly Asp Thr Ile Thr Gly Leu Asn Ala Ile Ile
 20 25 30
 Asn Glu Ala Phe Leu Gly Ile Pro Phe Ala Gln Pro Pro Val Gly Asn
 35 40 45
 Leu Arg Phe Lys Pro Pro Val Pro Tyr Ser Ala Ser Leu Asn Gly Gln
 50 55 60
 Lys Phe Thr Ser Tyr Gly Pro Ser Cys Met Gln Met Asn Pro Leu Gly
 65 70 75 80
 Asn Trp Asp Ser Ser Leu Pro Lys Ala Ala Ile Asn Ser Leu Met Gln
 85 90 95
 Ser Lys Leu Phe Gln Ala Val Leu Pro Asn Gly Glu Asp Cys Leu Thr
 100 105 110
 Ile Asn Val Val Arg Pro Ser Gly Thr Lys Pro Gly Ala Asn Leu Pro
 115 120 125
 Val Met Val Trp Ile Phe Gly Gly Gly Phe Glu Val Gly Gly Ser Ser
 130 135 140
 Leu Phe Pro Pro Ala Gln Met Ile Thr Ala Ser Val Leu Met Gly Lys
 145 150 155 160
 Pro Ile Ile His Val Ser Met Asn Tyr Arg Val Ala Ser Trp Gly Phe
 165 170 175
 Leu Ala Gly Pro Asp Ile Lys Ala Glu Gly Ser Gly Asn Ala Gly Leu
 180 185 190
 His Asp Gln Arg Leu Gly Leu Gln Trp Val Ala Asp Asn Ile Ala Gly
 195 200 205
 Phe Gly Gly Asp Pro Ser Lys Val Thr Ile Phe Gly Glu Ser Ala Gly
 210 215 220
 Ser Met Ser Val Met Cys Gln Leu Leu Trp Asn Asp Gly Asp Asn Thr
 225 230 235 240
 Tyr Asn Gly Lys Pro Leu Phe Arg Ala Ala Ile Met Gln Ser Gly Ala
 245 250 255
 Met Val Pro Ser Asp Pro Val Asp Gly Pro Tyr Gly Thr Gln Ile Tyr
 260 265 270
 Asp Gln Val Val Ala Ser Ala Gly Cys Gly Ser Ala Ser Asp Lys Leu
 275 280 285
 Ala Cys Leu Arg Ser Ile Ser Asn Asp Lys Leu Phe Gln Ala Thr Ser
 290 295 300
 Asp Thr Pro Gly Ala Leu Ala Tyr Pro Ser Leu Arg Leu Ser Phe Leu
 305 310 315 320
 Pro Arg Pro Asp Gly Thr Phe Ile Thr Asp Asp Met Phe Lys Leu Val
 325 330 335
 Arg Asp Gly Lys Cys Ala Asn Val Pro Val Ile Ile Gly Asp Gln Asn
 340 345 350
 Asp Glu Gly Thr Val Phe Ala Leu Ser Ser Leu Asn Val Thr Thr Asp
 355 360 365
 Ala Gln Ala Arg Gln Tyr Phe Lys Glu Ser Phe Ile His Ala Ser Asp
 370 375 380
 Ala Glu Ile Asp Thr Leu Met Ala Ala Tyr Pro Ser Asp Ile Thr Gln
 385 390 395 400
 Gly Ser Pro Phe Asp Thr Gly Ile Phe Asn Ala Ile Thr Pro Gln Phe

405 410 415
 Lys Arg Ile Ala Ala Val Leu Gly Asp Leu Ala Phe Thr Leu Pro Arg
 420 425 430
 Arg Tyr Phe Leu Asn His Phe Gln Gly Gly Thr Lys Tyr Ser Phe Leu
 435 440 445
 Ser Lys Gln Leu Ser Gly Leu Pro Val Ile Gly Thr His His Ala Asn
 450 455 460
 Asp Ile Val Trp Gln Asp Phe Leu Val Ser His Ser Ser Ala Val Tyr
 465 470 475 480
 Asn Asn Ala Phe Ile Ala Phe Ala Asn Asp Leu Asp Pro Asn Lys Ala
 485 490 495
 Gly Leu Leu Val Asn Trp Pro Lys Tyr Thr Ser Ser Ser Gln Ser Gly
 500 505 510
 Asn Asn Leu Leu Gln Ile Asn Ala Leu Gly Leu Tyr Thr Gly Lys Asp
 515 520 525
 Asn Phe Arg Thr Ala Gly Tyr Asp Ala Leu Phe Thr Asn Pro Ser Ser
 530 535 540
 Phe Phe Val
 545

<210> 7
 <211> 1641
 <212> DNA
 <213> Candida rugosa

<220>
 <221> CDS
 <222> (1)...(1641)

<400> 7
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 Ser Met Asn Ser Arg Gly Pro Ala Gly Arg Leu Gly Ser Val Pro Thr
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 gcc acg ctc gcc aac ggc gac acc atc acc ggt ctc aac gcc atc atc 96
 Ala Thr Leu Ala Asn Gly Asp Thr Ile Thr Gly Leu Asn Ala Ile Ile
 20 25 30

 aac gag gcg ttc ctc ggc att ccc ttt gcc gag ccg ccg gtg ggc aac 144
 Asn Glu Ala Phe Leu Gly Ile Pro Phe Ala Glu Pro Pro Val Gly Asn
 35 40 45

 ctc cgc ttc aag gac cct gtg ccg tac cgt ggg tct ctc aac ggt caa 192
 Leu Arg Phe Lys Asp Pro Val Pro Tyr Arg Gly Ser Leu Asn Gly Gln
 50 55 60

 tcc ttc acc gcg tac ggt ccg tct tgc atg cag cag aac ccc gag ggc 240
 Ser Phe Thr Ala Tyr Gly Pro Ser Cys Met Gln Gln Asn Pro Glu Gly
 65 70 75 80

 acc tac gag gag aac ctc ccc aag gtg gcg ctt gac ttg gtg atg cag 288
 Thr Tyr Glu Glu Asn Leu Pro Lys Val Ala Leu Asp Leu Val Met Gln
 85 90 95

 tcc aag gtg ttc cag gct gtt ctc ccc aac agc gag gac tgc ctc acc 336
 Ser Lys Val Phe Gln Ala Val Leu Pro Asn Ser Glu Asp Cys Leu Thr
 100 105 110

atc aac gtg gtg cgg ccg ccg ggc acc aag gcg ggc gcc aac ctc ccg Ile Asn Val Val Arg Pro Pro Gly Thr Lys Ala Gly Ala Asn Leu Pro 115 120 125	384
gtc atg ctc tgg atc ttt ggc ggt ggg ttt gag atc ggc agc ccc acc Val Met Leu Trp Ile Phe Gly Gly Gly Phe Glu Ile Gly Ser Pro Thr 130 135 140	432
atc ttc cct ccc gct cag atg gtc tcc aag agt gtg ctc atg ggc gag Ile Phe Pro Pro Ala Gln Met Val Ser Lys Ser Val Leu Met Gly Glu 145 150 155 160	480
ccc atc atc cac gtg gcc gtc aac tac cgc ttg gcg tcc ttt ggt ttc Pro Ile Ile His Val Ala Val Asn Tyr Arg Leu Ala Ser Phe Gly Phe 165 170 175	528
ttg gcc ggt ccg gac atc aag gcc gag ggc agc tcc aat gcc ggc ctc Leu Ala Gly Pro Asp Ile Lys Ala Glu Gly Ser Ser Asn Ala Gly Leu 180 185 190	576
aag gac cag cgc ttg ggc atg cag tgg gtg gca gac aac att gcc ggg Lys Asp Gln Arg Leu Gly Met Gln Trp Val Ala Asp Asn Ile Ala Gly 195 200 205	624
ttc ggc ggc gac ccg agc aag gtg acc atc ttt ggc gag tct gcg ggc Phe Gly Gly Asp Pro Ser Lys Val Thr Ile Phe Gly Glu Ser Ala Gly 210 215 220	672
agc atg tcc gtg ttg tgc cac ctt ctc tgg aat ggc ggc gac aac acg Ser Met Ser Val Leu Cys His Leu Leu Trp Asn Gly Gly Asp Asn Thr 225 230 235 240	720
tac aag ggc aag ccg ttg ttc cgc gcg ggc atc atg cag tct gga gcc Tyr Lys Gly Lys Pro Leu Phe Arg Ala Gly Ile Met Gln Ser Gly Ala 245 250 255	768
atg gtg ccg tct gac ccg gtg gac ggc acc tat gga gcc caa atc tat Met Val Pro Ser Asp Pro Val Asp Gly Thr Tyr Gly Ala Gln Ile Tyr 260 265 270	816
gac acg ttg gtg gct tct acg ggc tgc agc agt gcc agc aac aag ctt Asp Thr Leu Val Ala Ser Thr Gly Cys Ser Ser Ala Ser Asn Lys Leu 275 280 285	864
gcg tgc ttg cgt ggt ctt tct act cag gca ttg ctc gat gcc acc aac Ala Cys Leu Arg Gly Leu Ser Thr Gln Ala Leu Leu Asp Ala Thr Asn 290 295 300	912
gac acc cct ggg ttc ttg tcg tac acc tcg ttg cgg ttg tct tat ctc Asp Thr Pro Gly Phe Leu Ser Tyr Thr Ser Leu Arg Leu Ser Tyr Leu 305 310 315 320	960
ccg cgg ccc gac ggc gcc aac atc acc gat gac atg tac aag ttg gta Pro Arg Pro Asp Gly Ala Asn Ile Thr Asp Asp Met Tyr Lys Leu Val 325 330 335	1008

cgc gac ggc aag tat gca agc gtt ccc gtg atc att ggc gac cag aac Arg Asp Gly Lys Tyr Ala Ser Val Pro Val Ile Ile Gly Asp Gln Asn 340 345 350	1056
gac gag ggc ttc ttg ttt gat ctc tct tct ttg aac acc acc acc gag Asp Glu Gly Phe Leu Phe Asp Leu Ser Ser Leu Asn Thr Thr Thr Glu 355 360 365	1104
gcc gac gcc gag gca tac ctc aga aag tct ttc atc cac gcc acc gac Ala Asp Ala Glu Ala Tyr Leu Arg Lys Ser Phe Ile His Ala Thr Asp 370 375 380	1152
gcc gat atc acc gca ttg aag gcg gcg tac ccc agc gat gtc acc cag Ala Asp Ile Thr Ala Leu Lys Ala Ala Tyr Pro Ser Asp Val Thr Gln 385 390 395 400	1200
ggc tct ccg ttc gac acg ggc att ctc aac gcc ctt aca ccc cag ctc Gly Ser Pro Phe Asp Thr Gly Ile Leu Asn Ala Leu Thr Pro Gln Leu 405 410 415	1248
aag cgg atc aat gct gtg ctt ggc gac ctc acc ttt acc ctc tcg cgc Lys Arg Ile Asn Ala Val Leu Gly Asp Leu Thr Phe Thr Leu Ser Arg 420 425 430	1296
cgc tac ttc ctc aac cac tac acc ggt ggt ccc aag tac tcg ttc ctc Arg Tyr Phe Leu Asn His Tyr Thr Gly Gly Pro Lys Tyr Ser Phe Leu 435 440 445	1344
tct aag cag ctt tct ggg ttg ccc att ctc ggt acg ttc cac gcg aac Ser Lys Gln Leu Ser Gly Leu Pro Ile Leu Gly Thr Phe His Ala Asn 450 455 460	1392
gac att gtg tgg cag cac ttt ttg ttg ggc agc ggc agc gtc atc tac Asp Ile Val Trp Gln His Phe Leu Leu Gly Ser Gly Ser Val Ile Tyr 465 470 475 480	1440
aac aac gcg ttc atc gcg ttt gcc acc gac ttg gac ccc aac acc gcg Asn Asn Ala Phe Ile Ala Phe Ala Thr Asp Leu Asp Pro Asn Thr Ala 485 490 495	1488
ggc ttg tct gtg cag tgg ccc aag tac acc agc agc tct cag gcg ggg Gly Leu Ser Val Gln Trp Pro Lys Tyr Thr Ser Ser Ser Gln Ala Gly 500 505 510	1536
gac aac ttg atg cag atc agt gcc ttg ggc ttg tac acc ggc aag gac Asp Asn Leu Met Gln Ile Ser Ala Leu Gly Leu Tyr Thr Gly Lys Asp 515 520 525	1584
aac ttc cgc acc gcc ggc tac aac gct ttg ttt gcc gac ccg tct cac Asn Phe Arg Thr Ala Gly Tyr Asn Ala Leu Phe Ala Asp Pro Ser His 530 535 540	1632
ttt ttc gtg Phe Phe Val 545	1641

<210> 8
 <211> 547
 <212> PRT
 <213> Candida rugosa

<400> 8
 Ser Met Asn Ser Arg Gly Pro Ala Gly Arg Leu Gly Ser Val Pro Thr
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 Ala Thr Leu Ala Asn Gly Asp Thr Ile Thr Gly Leu Asn Ala Ile Ile
 20 25 30
 Asn Glu Ala Phe Leu Gly Ile Pro Phe Ala Glu Pro Pro Val Gly Asn
 35 40 45
 Leu Arg Phe Lys Asp Pro Val Pro Tyr Arg Gly Ser Leu Asn Gly Gln
 50 55 60
 Ser Phe Thr Ala Tyr Gly Pro Ser Cys Met Gln Gln Asn Pro Glu Gly
 65 70 75 80
 Thr Tyr Glu Glu Asn Leu Pro Lys Val Ala Leu Asp Leu Val Met Gln
 85 90 95
 Ser Lys Val Phe Gln Ala Val Leu Pro Asn Ser Glu Asp Cys Leu Thr
 100 105 110
 Ile Asn Val Val Arg Pro Pro Gly Thr Lys Ala Gly Ala Asn Leu Pro
 115 120 125
 Val Met Leu Trp Ile Phe Gly Gly Gly Phe Glu Ile Gly Ser Pro Thr
 130 135 140
 Ile Phe Pro Pro Ala Gln Met Val Ser Lys Ser Val Leu Met Gly Glu
 145 150 155 160
 Pro Ile Ile His Val Ala Val Asn Tyr Arg Leu Ala Ser Phe Gly Phe
 165 170 175
 Leu Ala Gly Pro Asp Ile Lys Ala Glu Gly Ser Ser Asn Ala Gly Leu
 180 185 190
 Lys Asp Gln Arg Leu Gly Met Gln Trp Val Ala Asp Asn Ile Ala Gly
 195 200 205
 Phe Gly Gly Asp Pro Ser Lys Val Thr Ile Phe Gly Glu Ser Ala Gly
 210 215 220
 Ser Met Ser Val Leu Cys His Leu Leu Trp Asn Gly Gly Asp Asn Thr
 225 230 235 240
 Tyr Lys Gly Lys Pro Leu Phe Arg Ala Gly Ile Met Gln Ser Gly Ala
 245 250 255
 Met Val Pro Ser Asp Pro Val Asp Gly Thr Tyr Gly Ala Gln Ile Tyr
 260 265 270
 Asp Thr Leu Val Ala Ser Thr Gly Cys Ser Ser Ala Ser Asn Lys Leu
 275 280 285
 Ala Cys Leu Arg Gly Leu Ser Thr Gln Ala Leu Leu Asp Ala Thr Asn
 290 295 300
 Asp Thr Pro Gly Phe Leu Ser Tyr Thr Ser Leu Arg Leu Ser Tyr Leu
 305 310 315 320
 Pro Arg Pro Asp Gly Ala Asn Ile Thr Asp Asp Met Tyr Lys Leu Val
 325 330 335
 Arg Asp Gly Lys Tyr Ala Ser Val Pro Val Ile Ile Gly Asp Gln Asn
 340 345 350
 Asp Glu Gly Phe Leu Phe Asp Leu Ser Ser Leu Asn Thr Thr Thr Glu
 355 360 365
 Ala Asp Ala Glu Ala Tyr Leu Arg Lys Ser Phe Ile His Ala Thr Asp
 370 375 380
 Ala Asp Ile Thr Ala Leu Lys Ala Ala Tyr Pro Ser Asp Val Thr Gln
 385 390 395 400
 Gly Ser Pro Phe Asp Thr Gly Ile Leu Asn Ala Leu Thr Pro Gln Leu

				405					410					415			
Lys	Arg	Ile	Asn	Ala	Val	Leu	Gly	Asp	Leu	Thr	Phe	Thr	Leu	Ser	Arg		
			420					425					430				
Arg	Tyr	Phe	Leu	Asn	His	Tyr	Thr	Gly	Gly	Pro	Lys	Tyr	Ser	Phe	Leu		
		435						440					445				
Ser	Lys	Gln	Leu	Ser	Gly	Leu	Pro	Ile	Leu	Gly	Thr	Phe	His	Ala	Asn		
	450					455					460						
Asp	Ile	Val	Trp	Gln	His	Phe	Leu	Leu	Gly	Ser	Gly	Ser	Val	Ile	Tyr		
465					470					475					480		
Asn	Asn	Ala	Phe	Ile	Ala	Phe	Ala	Thr	Asp	Leu	Asp	Pro	Asn	Thr	Ala		
			485						490					495			
Gly	Leu	Ser	Val	Gln	Trp	Pro	Lys	Tyr	Thr	Ser	Ser	Ser	Gln	Ala	Gly		
			500					505					510				
Asp	Asn	Leu	Met	Gln	Ile	Ser	Ala	Leu	Gly	Leu	Tyr	Thr	Gly	Lys	Asp		
		515					520					525					
Asn	Phe	Arg	Thr	Ala	Gly	Tyr	Asn	Ala	Leu	Phe	Ala	Asp	Pro	Ser	His		
	530					535					540						
Phe	Phe	Val															
545																	

<210> 9

<211> 1641

<212> DNA

<213> *Candida rugosa*

<220>

<221> CDS

<222> (1)...(1641)

<400> 9

tcg	atg	aat	tca	cgt	ggc	cca	gcc	ggc	cgt	ctc	gga	tcg	gta	ccc	act		48
Ser	Met	Asn	Ser	Arg	Gly	Pro	Ala	Gly	Arg	Leu	Gly	Ser	Val	Pro	Thr		
1				5					10					15			
gcc	acg	ctc	gcc	aac	ggc	gac	acc	atc	acc	ggg	ctc	aac	gcc	atc	atc		96
Ala	Thr	Leu	Ala	Asn	Gly	Asp	Thr	Ile	Thr	Gly	Leu	Asn	Ala	Ile	Ile		
			20					25					30				
aac	gag	gcg	ttc	ctc	ggc	att	ccc	ttt	gcc	gag	ccg	ccg	gtg	ggc	aac		144
Asn	Glu	Ala	Phe	Leu	Gly	Ile	Pro	Phe	Ala	Glu	Pro	Pro	Val	Gly	Asn		
		35					40					45					
ctc	cgc	ttc	aag	gac	ccc	gtg	ccg	tac	tcc	ggc	tcg	ctc	gat	ggc	cag		192
Leu	Arg	Phe	Lys	Asp	Pro	Val	Pro	Tyr	Ser	Gly	Ser	Leu	Asp	Gly	Gln		
		50				55					60						
aag	ttc	act	tct	tac	ggc	ccg	tct	tgc	atg	cag	cag	aac	ccc	gag	ggc		240
Lys	Phe	Thr	Ser	Tyr	Gly	Pro	Ser	Cys	Met	Gln	Gln	Asn	Pro	Glu	Gly		
	65				70				75					80			
acc	tac	gag	gag	aac	ctc	ccc	aag	gca	gcg	ctc	gac	ttg	gtg	atg	cag		288
Thr	Tyr	Glu	Glu	Asn	Leu	Pro	Lys	Ala	Ala	Leu	Asp	Leu	Val	Met	Gln		
				85				90						95			
tcc	aag	gtg	ttt	gag	gcg	gtg	tct	ccg	tct	agc	gag	gac	tgt	ctc	acc		336
Ser	Lys	Val	Phe	Glu	Ala	Val	Ser	Pro	Ser	Ser	Glu	Asp	Cys	Leu	Thr		
			100					105					110				

atc aac gtg gtg cgg ccg ccg ggc acc aag gcg ggt gcc aac ctc ccg	384
Ile Asn Val Val Arg Pro Pro Gly Thr Lys Ala Gly Ala Asn Leu Pro	
115 120 125	
gtg atg ctc tgg atc ttt ggc ggc ggg ttt gag gtg ggt ggc acc agc	432
Val Met Leu Trp Ile Phe Gly Gly Gly Phe Glu Val Gly Gly Thr Ser	
130 135 140	
acc ttc cct ccc gcc cag atg atc acc aag agc att gcc atg ggc aag	480
Thr Phe Pro Pro Ala Gln Met Ile Thr Lys Ser Ile Ala Met Gly Lys	
145 150 155 160	
ccc atc atc cac gtg agc gtc aac tac cgc gtg tcg tcg tgg ggg ttc	528
Pro Ile Ile His Val Ser Val Asn Tyr Arg Val Ser Ser Trp Gly Phe	
165 170 175	
ttg gct ggc gac gag atc aag gcc gag ggc agt gcc aac gcc ggt ttg	576
Leu Ala Gly Asp Glu Ile Lys Ala Glu Gly Ser Ala Asn Ala Gly Leu	
180 185 190	
aag gac cag cgc atg ggc atg cag tgg gtg gcg gac aac att gcg gcg	624
Lys Asp Gln Arg Met Gly Met Gln Trp Val Ala Asp Asn Ile Ala Ala	
195 200 205	
ttt ggc ggc gac ccg acc aag gtg acc atc ttt ggc gag tct gcg ggc	672
Phe Gly Gly Asp Pro Thr Lys Val Thr Ile Phe Gly Glu Ser Ala Gly	
210 215 220	
agc atg tcg gtc atg tgc cac att ctc tgg aac gac ggc gac aac acg	720
Ser Met Ser Val Met Cys His Ile Leu Trp Asn Asp Gly Asp Asn Thr	
225 230 235 240	
tac aag ggc aag ccg ctc ttc cgc gcg ggc atc atg cag tct ggg gcc	768
Tyr Lys Gly Lys Pro Leu Phe Arg Ala Gly Ile Met Gln Ser Gly Ala	
245 250 255	
atg gta ccg tcg gac gcg gtg gac ggc gtc tac ggc aac gag atc ttt	816
Met Val Pro Ser Asp Ala Val Asp Gly Val Tyr Gly Asn Glu Ile Phe	
260 265 270	
gac ctc ttg gcg tcg gac gcg ggc tgc ggc agc gcc agc gac aag ctt	864
Asp Leu Leu Ala Ser Asp Ala Gly Cys Gly Ser Ala Ser Asp Lys Leu	
275 280 285	
gcg tgc ttg cgc ggt gtg tct agc gac acg ttg gag gac gcc acc aac	912
Ala Cys Leu Arg Gly Val Ser Ser Asp Thr Leu Glu Asp Ala Thr Asn	
290 295 300	
aac acc cct ggg ttc ttg gcg tac tcc tcg ttg cgg ttg tct tat ctc	960
Asn Thr Pro Gly Phe Leu Ala Tyr Ser Ser Leu Arg Leu Ser Tyr Leu	
305 310 315 320	
ccg cgg ccc gac ggc gtg aac atc acc gac gac atg ttt gcc ttg gtc	1008
Pro Arg Pro Asp Gly Val Asn Ile Thr Asp Asp Met Phe Ala Leu Val	
325 330 335	

cgc gag ggc aag tat gca agc gtt cct gtg atc atc ggc gac cag aac	1056
Arg Glu Gly Lys Tyr Ala Ser Val Pro Val Ile Ile Gly Asp Gln Asn	
340 345 350	
gac gag ggc acc ttc ttt ggc acc tct tct ttg aac gtg acc acg gat	1104
Asp Glu Gly Thr Phe Phe Gly Thr Ser Ser Leu Asn Val Thr Thr Asp	
355 360 365	
gcc gag gcc cgc cag tac ttc acg cag tct ttt gtc cac gcc agc gac	1152
Ala Glu Ala Arg Gln Tyr Phe Thr Gln Ser Phe Val His Ala Ser Asp	
370 375 380	
gcg gag ctc gac acg ttg atg acg gcg tac ccc cag gac atc acc cag	1200
Ala Glu Leu Asp Thr Leu Met Thr Ala Tyr Pro Gln Asp Ile Thr Gln	
385 390 395 400	
ggg tct ccg ttc gac acg ggt gtt ctc aac gcc ctc acc ccg cag ttc	1248
Gly Ser Pro Phe Asp Thr Gly Val Leu Asn Ala Leu Thr Pro Gln Phe	
405 410 415	
aag aga atc tct gcg gtg ctc ggc gac ctt gcc ttc atc cac gcc cgt	1296
Lys Arg Ile Ser Ala Val Leu Gly Asp Leu Ala Phe Ile His Ala Arg	
420 425 430	
cgc tac ttc ctc aac cac tac acc ggc ggc acc aag tac tca ttc ctc	1344
Arg Tyr Phe Leu Asn His Tyr Thr Gly Gly Thr Lys Tyr Ser Phe Leu	
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tct aag cag ctc tct ggc ttg ccg gtg ctc gga acg ttc cac tcc aac	1392
Ser Lys Gln Leu Ser Gly Leu Pro Val Leu Gly Thr Phe His Ser Asn	
450 455 460	
gac att gtc ttc cag gac tac ttg ttg ggc agc ggc tcg ctc atc tac	1440
Asp Ile Val Phe Gln Asp Tyr Leu Leu Gly Ser Gly Ser Leu Ile Tyr	
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Asn Asn Ala Phe Ile Ala Phe Ala Thr Asp Leu Asp Pro Asn Thr Ala	
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ggg ttg ttg gtg aag tgg ccc gag tac acc agc agc tct cag tct ggc	1536
Gly Leu Leu Val Lys Trp Pro Glu Tyr Thr Ser Ser Ser Gln Ser Gly	
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aac aac ttg atg atg atc aac gcc ttg ggc ttg tac acc ggc aag gac	1584
Asn Asn Leu Met Met Ile Asn Ala Leu Gly Leu Tyr Thr Gly Lys Asp	
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Asn Ser Arg Thr Ala Gly Tyr Asp Ala Leu Phe Ser Asn Pro Pro Ser	
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ttc ttt gtg	1641
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Pro	Ile	Ile	His	Val	Ser	Val	Asn	Tyr	Arg	Val	Ser	Ser	Trp	Gly	Phe
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Ser Met Asn Ser Arg Gly Pro Ala Gly Arg Leu Gly Ser

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